What is claimed is:

1. A method, comprising the steps of:

detecting an expression profile of at least one gene in a biological sample of a subject; and

comparing said expression profile to a reference expression profile of said at least one gene,

wherein said at least one gene is differentially expressed in at least two types of cancer cells as compared to corresponding cancer-free cells.

2. The method of claim 1, wherein each of said at least two types is selected from the group consisting of colon cancer, lung cancer, breast cancer, and prostate cancer.

3. The method of claim 2, wherein said at least one gene includes at least one kinase gene which is overexpressed in said at least two types of cancer cells as compared to said corresponding cancer-free cells.

4. The method of claim 2, wherein said at least one gene includes one or more genes selected from Table 1.

5. The method of claim 2, wherein the biological sample is a colon sample, a lung sample, a breast sample, or a prostate sample, and said reference expression profile is an average expression profile of said at least one gene in reference biological samples of cancer-free subjects.

6. The method of claim 5, wherein said expression profile and said reference expression profile are determined using RT-PCR, nucleic acid arrays, or immunoassays.

7. The method of claim 2, wherein said subject has colon cancer, lung cancer, breast cancer, or prostate cancer.

8. A method comprising:

detecting an expression profile of at least one gene in a biological sample of a subject; and

comparing said expression profile to a reference expression profile of said at least one gene,

wherein said at least one gene has a statistically significant T score under a contrast analysis, wherein the contrast analysis is capable of comparing average expression levels of said at least one gene in at least four sample sets to a predetermined pattern, wherein

said at least four sample sets include a first pair and a second pair of sample sets, the first pair of sample sets including a set of samples having a first cancer and a set of samples free of the first cancer, the second pair of sample sets including a set of samples having a second cancer and a set of samples free of the second cancer, and wherein said predetermined pattern is defined as "high in cancer sample set, low in cancer-free set" or "low in cancer sample set, high in cancer-free set."

9. A method, comprising the steps of:

detecting in a biological sample the level of T cells that are activated by one or more polypeptides encoded by at least one gene which is differentially expressed in at least two types of cancer cells as compared to corresponding cancer-free cells; and

comparing the level to a reference level of said T cells.

10. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and at least one component selected from the group consisting of:

a polypeptide encoded by a gene which is over-expressed in at least two types of cancer cells as compared to corresponding cancer-free cells;

a variant of said polypeptide; and

a polynucleotide encoding said polypeptide or said variant.

11. The pharmaceutical composition of claim 10, wherein the pharmaceutical composition is a vaccine formulation capable of eliciting an immune response against a cancer cell or a component thereof, and wherein said gene is selected from Table 1.

12. A method comprising administering an immunoeffective amount of the pharmaceutical composition of claim 11 to a subject in need thereof.

13. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and at least one component selected from the group consisting of:

an agent capable of modulating the expression of a gene which is over-expressed in at least two types of cancer cells as compared to corresponding cancer-free cells;

an agent capable of binding to, or modulating an activity of, a polypeptide encoded by said gene; and

a T cell activated by said polypeptide.

14. The pharmaceutical composition of claim 13, wherein said component is selected from the group consisting of:

a polynucleotide comprising or encoding an RNA that is capable of inhibiting or decreasing the expression of said gene by RNA interference or an antisense mechanism;

an antibody specific for said polypeptide encoded by said gene; and

an inhibitor of a biological activity of said polypeptide, wherein said gene is selected from Table 1.

15. A method comprising administering the pharmaceutical composition of claim 14 to a subject who has colon cancer, lung cancer, breast cancer, or prostate cancer.

16. The pharmaceutical composition of claim 13, wherein said component is a polynucleotide comprising or encoding a siRNA sense or antisense sequence selected from Table 4.

17. A nucleic acid array comprising one or more substrate supports which are stably associated with polynucleotide probes, wherein a substantial portion of all polynucleotide probes that are stably associated with said one or more substrate supports are capable of hybridizing under reduced stringent, stringent or highly stringent conditions to RNA transcripts, or the complements thereof, of genes which are differentially expressed in at least two types of cancer cells as compared to corresponding cancer-free cells.

18. A polypeptide array comprising one or more substrate supports which are stably associated with a plurality of polypeptides, wherein a substantial portion of all polypeptides that are stably associated with said one or more substrate supports consists of:

polypeptides encoded by genes which are differentially expressed in at least two types of cancer cells as compared to corresponding cancer-free cells;

variants of said polypeptides;

antibodies specific for said polypeptides or variants;

or any combination of said polypeptides, variants or antibodies.

19. A cancer diagnostic kit comprising at least one of:

a polynucleotide probe capable of specifically binding to a sequence recited in any one of SEQ ID NOS:1-44 or the complement thereof; and

an antibody capable of specifically binding to a polypeptide sequence recited in any one of SEQ ID NOS:45-88.

20. A method for identifying an agent capable of modulating an activity of a gene which is differentially expressed in at least two types of cancer cells as compared to corresponding cancer-free cells, said method comprising:

contacting a candidate agent with a polypeptide encoded by said gene;

comparing a biological activity of said polypeptide in the presence and absence of said candidate agent to determine if said candidate agent can modulate said biological activity.